ABSTRACT

The present invention provides methionine aminopeptidases (MetAPs) with a broad substrate range, particularly those capable of removing the N-terminal Met from bulky or acidic penultimate residues. In preferred embodiments, these MetAPs have mutations at the 233, 206 and/or 168 positions of SEQ ID NO:1. Preferably, amino acids at these residues are substituted with glycine or threonine. Also provided are cells comprising the MetAPs, DNA encoding the MetAPs, and methods of using the MetAPs.